

OIPE

#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/837,446

DATE: 05/07/2001
 TIME: 17:55:04

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\05072001\I837446.raw

4 <110> APPLICANT: Butcher, Eugene C.
 5 Campbell, James J.
 6 Rottman, James B.
 7 Wu, Lijan
 9 <120> TITLE OF INVENTION: Modulation of Systemic Memory T Cell
 10 Trafficking
 12 <130> FILE REFERENCE: STAN-110CON
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/837,446
 15 <141> CURRENT FILING DATE: 2001-04-17
 17 <150> PRIOR APPLICATION NUMBER: 09/232,878
 18 <151> PRIOR FILING DATE: 1999-01-15
 20 <160> NUMBER OF SEQ ID NOS: 6
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1677
 26 <212> TYPE: DNA
 27 <213> ORGANISM: H. sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (183)...(1265)
 32 <223> OTHER INFORMATION: CCR4, Chemokine receptor coding sequence
 34 <400> SEQUENCE: 1
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 36 tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc 120
 37 agaaaagcaa gctgcttctg gttgggcccac gacctgcctt gaggagcctg tagagttaaa 180
 38 aa`atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
 39 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
 40 1 5 10 15 275
 42 tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa
 43 Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
 44 20 25 30
 46 gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
 47 Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
 48 35 40 45
 50 ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
 51 Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
 52 50 55 60
 54 ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
 55 Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
 56 65 70 75
 58 aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467
 59 Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
 60 80 85 90
 62 ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515
 63 Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
 64 100 105 110
 66 atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563

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67	Met	Ile	Ser	Trp	Met	Tyr	Leu	Val	Gly	Phe	Tyr	Ser	Gly	Ile	Phe	Phe	
68				115					120					125			
70	gtc	atg	ctc	atg	agc	att	gat	aga	tac	ctg	gcg	ata	gtg	cac	gcg	gtg	611
71	Val	Met	Leu	Met	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	
72			130					135					140				
74	ttt	tcc	ttg	agg	gca	agg	acc	ttg	act	tat	ggg	gtc	atc	acc	agt	ttg	659
75	Phe	Ser	Leu	Arg	Ala	Arg	Thr	Leu	Thr	Tyr	Gly	Val	Ile	Thr	Ser	Leu	
76		145				150					155						
78	gct	aca	tgg	tca	gtg	gct	gtg	ttc	gcc	tcc	ctt	cct	ggc	ttt	ctg	ttc	707
79	Ala	Thr	Trp	Ser	Val	Ala	Val	Phe	Ala	Ser	Leu	Pro	Gly	Phe	Leu	Phe	
80	160				165					170				175			
82	agc	act	tgt	tat	act	gag	cgc	aac	cat	acc	tac	tgc	aaa	acc	aag	tac	755
83	Ser	Thr	Cys	Tyr	Thr	Glu	Arg	Asn	His	Thr	Tyr	Cys	Lys	Thr	Lys	Tyr	
84			180					185						190			
86	tct	ctc	aac	tcc	acg	acg	tgg	aag	gtt	ctc	agc	tcc	ctg	gaa	atc	aac	803
87	Ser	Leu	Asn	Ser	Thr	Thr	Trp	Lys	Val	Leu	Ser	Ser	Leu	Glu	Ile	Asn	
88			195					200					205				
90	att	ctc	gga	ttg	gtg	atc	ccc	tta	ggg	atc	atg	ctg	ttt	tgc	tac	tcc	851
91	Ile	Leu	Gly	Leu	Val	Ile	Pro	Leu	Gly	Ile	Met	Leu	Phe	Cys	Tyr	Ser	
92			210				215					220					
94	atg	atc	atc	agg	acc	ttg	cag	cat	tgt	aaa	aat	gag	aag	aag	aac	aag	899
95	Met	Ile	Ile	Arg	Thr	Leu	Gln	His	Cys	Lys	Asn	Glu	Lys	Lys	Asn	Lys	
96		225				230				235							
98	gcg	gtg	aag	atg	atc	ttt	gcc	gtg	gtg	gtc	ctc	ttc	ctt	ggg	ttc	tgg	947
99	Ala	Val	Lys	Met	Ile	Phe	Ala	Val	Val	Leu	Phe	Leu	Gly	Phe	Trp		
100	240				245					250			255				
102	aca	cct	tac	aac	ata	gtg	ctc	ttc	cta	gag	acc	ctg	gtg	gag	cta	gaa	995
103	Thr	Pro	Tyr	Asn	Ile	Val	Leu	Phe	Leu	Glu	Thr	Leu	Val	Glu	Leu	Glu	
104				260					265				270				
106	gtc	ctt	cag	gac	tgc	acc	ttt	gaa	aga	tac	ttg	gac	tat	gcc	atc	cag	1043
107	Val	Leu	Gln	Asp	Cys	Thr	Phe	Glu	Arg	Tyr	Leu	Asp	Tyr	Ala	Ile	Gln	
108			275					280				285					
110	gcc	aca	gaa	act	ctg	gct	ttt	gtt	cac	tgc	tgc	ctt	aat	ccc	atc	atc	1091
111	Ala	Thr	Glu	Thr	Leu	Ala	Phe	Val	His	Cys	Cys	Leu	Asn	Pro	Ile	Ile	
112		290					295				300						
114	tac	ttt	ttt	ctg	ggg	gag	aaa	ttt	cgc	aag	tac	atc	cta	cag	ctc	ttc	1139
115	Tyr	Phe	Phe	Leu	Gly	Glu	Lys	Phe	Arg	Lys	Tyr	Ile	Leu	Gln	Leu	Phe	
116		305				310				315							
118	aaa	acc	tgc	agg	ggc	ctt	ttt	gtg	ctc	tgc	caa	tac	tgt	ggg	ctc	ctc	1187
119	Lys	Thr	Cys	Arg	Gly	Leu	Phe	Val	Leu	Cys	Gln	Tyr	Cys	Gly	Leu	Leu	
120	320				325				330			335					
122	caa	att	tac	tct	gct	gac	acc	ccc	agc	tca	tct	tac	acg	cag	tcc	acc	1235
123	Gln	Ile	Tyr	Ser	Ala	Asp	Thr	Pro	Ser	Ser	Ser	Tyr	Thr	Gln	Ser	Thr	
124			340					345			350						
126	atg	gat	cat	gat	ctt	cat	gat	gct	ctg	tag	gaaaaatgaa	atggtgaaat					1285
127	Met	Asp	His	Asp	Leu	His	Asp	Ala	Leu	*							
128			355					360									
130	gcagagtcaa	tgaacttttc	cacattcaga	gcttacttta	aaattggtat	ttttaggtaa											1345
131	gagatccctg	agccagtgtc	aggaggaagg	cttacacca	cagtggaaag	acagcttctc											1405

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132 atcctgcagg cagctttttc tctcccacta gacaagtcca gcctggcaag ggttcacctg 1465
133 ggctgaggca tccttctca caccaggctt gcctgcaggc atgagtcagt ctgatgagaa 1525
134 ctctgagcag tgcttgaatg aagttgtagg taatattgca aggcaaagac tattcccttc 1585
135 taacctgaac tgatggggtt ctccagaggg aattgcagag tactggctga tggagtaaatt 1645
136 cgctaccttt tgctgtggca aatgggcccc cg 1677
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 360
140 <212> TYPE: PRT
141 <213> ORGANISM: H. sapiens
143 <400> SEQUENCE: 2
144 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
145 1 5 10 15
146 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
147 20 25 30
148 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
149 35 40 45
150 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
151 50 55 60
152 Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
153 65 70 75 80
154 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
155 85 90 95
156 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
157 100 105 110
158 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
159 115 120 125
160 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
161 130 135 140
162 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
163 145 150 155 160
164 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 165 170 175
166 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
167 180 185 190
168 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
169 195 200 205
170 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
171 210 215 220
172 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
173 225 230 235 240
174 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
175 245 250 255
176 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
177 260 265 270
178 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
179 275 280 285
180 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
181 290 295 300
182 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys

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183 305
184 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
185 325 330 335
186 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
187 340 345 350
188 Asp His Asp Leu His Asp Ala Leu
189 355 360
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 538
193 <212> TYPE: DNA
194 <213> ORGANISM: H. sapiens
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (53)...(337)
199 <223> OTHER INFORMATION: Coding sequence for TARC chemokine
201 <400> SEQUENCE: 3
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203 Met Ala
204 1
206 cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
207 Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
208 5 10 15
210 cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
211 Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
212 20 25 30
214 ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
215 Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
216 35 40 45 50
218 tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
219 Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
220 55 60 65
222 gtg cag ggc agg gcc atc tgt tgc gac ccc aac aac aag aga gtg aag 298
223 Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
224 70 75 80
226 aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga' agcctcctca 347
227 Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser *
228 85 90
230 cccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tgttcaccgc 407
231 cccaccctg agcgctggg tccaggggag gccttccagg gacgaagaag agccacagtg 467
232 agggagatcc catccccttg tctgaactgg agccatgggc acaaagggcc cagattaaag 527
233 tctttatcct c 538
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 94
237 <212> TYPE: PRT
238 <213> ORGANISM: H. sapiens
240 <400> SEQUENCE: 4
241 Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
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243 Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu

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244          20          25          30
245 Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
246          35          40          45
247 Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
248          50          55          60
249 Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
250 65          70          75          80
251 Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
252          85          90
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 2923
256 <212> TYPE: DNA
257 <213> ORGANISM: H. sapiens
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (20)...(301)
262 <223> OTHER INFORMATION: Coding sequence for MDC chemokine
264 <400> SEQUENCE: 5
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266          Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val
267          1          5          10
269 ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100
270 Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
271          15          20          25
273 ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
274 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
275          30          35          40
277 cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
278 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
279          45          50          55
281 tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc 244
282 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
283 60          65          70          75
285 tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
286 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
287          80          85          90
289 agc caa tga' agagcctact ctgatgaccg tggccttgcc tctccagga 341
290 Ser Gln *
293 aggetcagga gccctacctc cctgccatta tagctgctcc ccgccagaag cctgtgccaa 401
294 ctctctgcat tccctgatct ccatccctgt ggctgtcacc cttggtcacc tccgtgctgt 461
295 cactgccatc tccccctga cccctctaac ccatcctctg cctccctccc tgcagtcaga 521
296 gggctcctgtt cccatcagcg attccccctgc ttaaaccctt ccatgactcc ccaactgccct 581
297 aagctgaggt cagtctccca agcctggcat gtggccctct ggatctgggt tccatctctg 641
298 tctccagcct gccacttcc ctccatgaat gttgggttct agctccctgt tctccaaacc 701
299 catactacac atcccacttc tgggtotttg cctgggatgt tgctgacact cagaaagtcc 761
300 caccacctgc acatgtgtag ccccaccagc cctccaaggc attgctcgcc caagcagctg 821
301 gtaattccat ttcattgtatt agatgtcccc tggccctctg tcccccttta ataaccctag 881
302 tcacagtctc cgcagattct tgggatttgg gggttttctc cccacctct ccaactagttg 941
303 gaccaaggtt tctagctaa' ttactctagt ctccaagcct ctagcataga gcaactgcaga 1001

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VERIFICATION SUMMARY

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DATE: 05/07/2001

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Input Set : A:\Seqlist.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number